A systems biology approach to unravel the effects of cadmium exposure on Arabidopsis thaliana

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A systems biology approach to unravel the effects of cadmium exposure on *Arabidopsis thaliana*.

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Introduction

Cadmium (Cd) is a biologically non-essential, toxic, metallic trace element. It is a **pollutant** which mostly accumulates in soils due to mining, metal industry, waste incineration, and the application of phosphate fertilizers. In plants, Cd leads to **decreased yield** and, eventually, death. Furthermore, Cd enters the food chain through plants to reach food and feed, in which it has detrimental effects for animal and human health. Cleansing of contaminated soils by phytoremediation has been proposed, but due to the negative effects of Cd in plants, such as the induction of **oxidative stress**, it is necessary to have a thorough understanding of the **underlying molecular responses of plants to Cd exposure.**

Fig. 1: Cadmium (Source: Wikipedia)

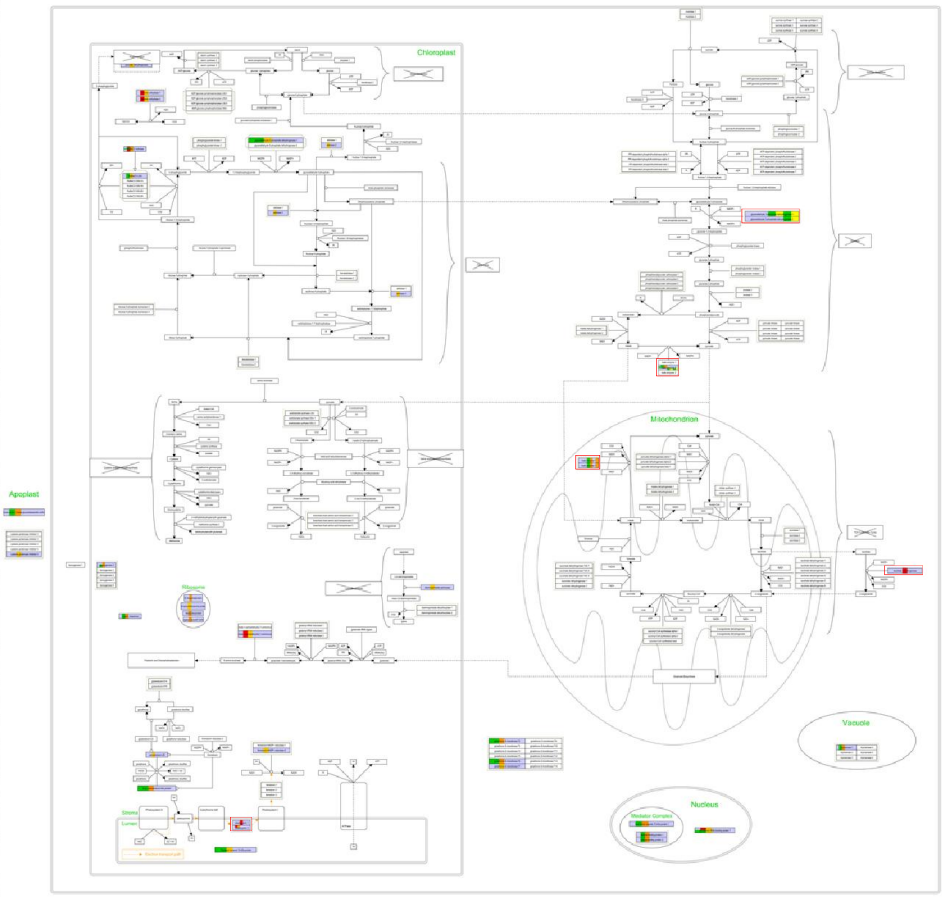
Materials and Methods

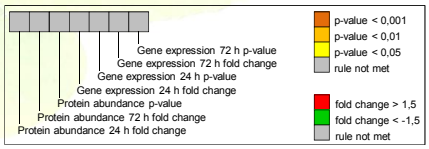
- ***Arabidopsis thaliana*** (Columbia) plants were grown in a **hydroponics** system (Hoogland). After 19 days of growth **5 µM $CdSO_4$** was added to the nutrient solution of treated plants. Control and treated Arabidopsis **rosettes** of were harvested after **0, 24 h and 72 h** of treatment (Fig. 2).
- **Proteins** were extracted using TCA/acetone and separated by **different gel electrophoresis (DiGE)**. **Genes of interes**t were selected according to the proteomics results and transcript abundance was measured by **qPCR** (Fig. 3).
- **Proteomics and transcriptomics data was integratively visualized** on the Arabidopsis **Primary Plant Metabolism pathway** drawn using PathViso and shared on WikiPathways **(WP2499)** (Fig. 4).

Visible Symptoms

Fig. 2: After only 72 hours of treatment clear signs of stress were visible in the form of **necroses on leaves**.

Representation of Omics Data





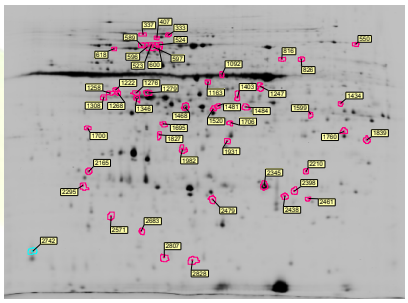


Fig. 2: 2DE gel image of the internal standard showing identified differentially abundant proteins.

Discussion

- **Differentially abundant proteins** were mostly involved in **primary carbon metabolism, photosynthesis, and glutathione based detoxification**.
- Transcriptomics data was mostly confirmatory of the Proteomics results.
- Many of the proteins of interest use **NAD/NADH** or **NADP/NADPH** as a cofactor. NADH and NADPH are the most important carriers of **reducing power** and of utter importance during oxidative stress. Furthermore this is an indication of the importance of redox regulation.

Fig. 4: Proteomics and transcriptomics data visualized on the Arabidopsis Primary Plant Metabolism pathway (WP2499).